STIC Search Report
Biotech-Chem Library

USPTO

STIC Database Tracking Number: 145470

TO: David Lamberston
Location: rem/2b79/2c70
Art Unit: 1636
Thursday, February 17, 2005

Case Serial Number: 09/974760

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518

barbara.obryen@uspto.gov

Search Notes

sira
Search and Information
Resources Administration

```
                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:    February 15, 2005, 01:46:24 ; Search time 168 Seconds
                                (without alignments)
                         1079.706 Million cell updates/sec

Title:          US-09-974-760B-91
Perfect score:  2456
Sequence:       1 MAADQGIFTNSVTLSPVEGS.........FSLARKHKHGMLRDLNNIPP 469

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:    2105643

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 95%
                 Listing first 45 summaries

Database :    A_Geneseq_16Dec04:*
              1: geneseqp1980s:*
              2: geneseqp1990s:*
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              4: geneseqp2001s:*
              5: geneseqp2002s:*
              6: geneseqp2003as:*
              7: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match Length	DB	ID	Description
1	2035	82.9	469	6	ABR64151	Abr64151 Aspergill
2	830	33.8	459	7	AAU10871	Aau10871 Penicilli
3	830	33.8	459	7	ADE81191	Ade81191 MicR, SEQ
4	157.5	6.4	424	5	ABP63135	Abp63135 lovF gene
5	157.5	6.4	424	5	ABP35719	Abp35719 Fungal ZB
6	154.5	6.3	919	5	ABP35687	Abp35687 Fungal ZB
7	154.5	6.3	919	8	ADN18782	Adn18782 Bacterial
8	141	5.7	727	2	ADC52108	Adc52108 A. oryzae
9	136	5.5	604	2	AAW37163	Aaw37163 Aspergill
10	136	5.5	604	5	ABP35591	Abp35591 Fungal ZB
11	135	5.5	433	5	ABP35583	Abp35583 Fungal ZB
12	132	5.5	1170	5	ABP35667	Abp35667 Fungal ZB
13	132	5.4	1170	8	ADS43829	Ads43829 Bacterial
14	131.5	5.4	480	5	ABP35612	Abp35612 Fungal ZB
15	130.5	5.3	662	5	ABP35590	Abp35590 Fungal ZB
16	130.5	5.3	792	5	ABG93477	Abg93477 Aspergill
17	129.5	5.3	579	5	ABP35589	Abp35589 Fungal ZB
18	126.5	5.2	341	2	AAW58573	Aaw58573 Trichoder
19	126	5.1	821	5	ABG93475	Abg93475 Aspergill
20	124.5	5.1	736	5	ABP35614	Abp35614 Fungal ZB
21	124	5.0	984	5	ABP35627	Abp35627 Fungal ZB
22	123.5	5.0	437	5	ABP35582	Abp35582 Fungal ZB
23	123.5	5.0	607	5	ABP35705	Abp35705 Fungal ZB
24	122	5.0	821	5	ABG93469	Abg93469 Aspergill
25	122	5.0	821	5	ABP35586	Abp35586 Fungal ZB
26	121.5	4.9	964	4	AAB30811	Amino aci
27	121.5	4.9	964	5	ABP35696	Fungal ZB
28	121.5	4.9	964	7	ADK62832	Disease t
29	121	4.9	470	5	ABP35710	Fungal ZB
30	121	4.9	739	5	ABP35675	Fungal ZB
31	121	4.9	821	5	ABG93472	Aspergill
32	120.5	4.9	532	7	ADE81193	Orf1, SEQ
33	120.5	4.9	795	5	ABG93476	Aspergill
34	120	4.9	470	5	ABP35648	Fungal ZB
35	119.5	4.9	999	7	ABR84508	Human ani
36	119.5	4.8	999	7	ABR84509	Mouse ani
37	119.5	4.8	470	5	ABP35652	Fungal ZB
38	119	4.8	565	5	ABP35662	Fungal ZB
39	119	4.8	630	7	ADE71247	Novel hum
40	119	4.8	631	8	ABO84656	Human can
41	119	4.8	703	8	ABO84655	Human can
42	119	4.8	1163	8	ADQ65188	Novel hum
43	119	4.8	1331	8	ADR10449	Human pro
44	118.5	4.8	857	5	ABP35608	Fungal ZB
45	118.5	4.8	2016	6	AAE36891	Plectreur

ALIGNMENTS

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ID   ABR64151 standard; protein; 469 AA.
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AC   ABR64151;
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DT   15-OCT-2003  (first entry)
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DE   Aspergillus terreus lovE protein mutant sequence.
XX
KW   LovE; regulator; wild-type; fungus; secondary metabolite; lovastatin;
KW   food additive; vitamin; mutant; mutein.
XX
OS   Aspergillus terreus.
XX
FH   Key            Location/Qualifiers
FT   Misc-difference 4
FT                  /note= "Asp at this position in wild type protein"
FT   Misc-difference 9
FT                  /note= "Thr at this position in wild type protein"
FT   Misc-difference 14
FT                  /note= "Leu at this position in wild type protein"
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FT   Misc-difference 62
FT                  /note= "Gln at this position in wild type protein"
FT   Misc-difference 73
FT                  /note= "Cys at this position in wild type protein"
FT   Misc-difference 77
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FT   Misc-difference 80
FT                  /note= "Gln at this position in wild type protein"
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OM protein - protein search, using sw model

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                  GenCore version 5.1.6
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Run on: February 15, 2005, 01:57:35 ; Search time 43 Seconds
                                          (without alignments)
                                814.196 Million cell updates/sec

Title: US-09-974-760B-91
Perfect score: 2456
Sequence: 1 MAADQGIFTNSVTLSPVEGS.........FSLARKHKHGMLRDLNNIPP 469

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 95%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
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             2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
             3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
             4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
             5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB	ID	Description
1	157.5	6.4	424	4	US-10-029-180-104	Sequence 104, App
2	136	5.5	604	4	US-09-197-814-3	Sequence 3, Appli
3	136	5.5	604	4	US-09-920-581-3	Sequence 3, Appli
4	119	4.8	631	3	US-09-147-119-7	Sequence 7, Appli
5	119	4.8	707	4	US-09-949-016-8495	Sequence 8495, Ap
6	118	4.8	439	4	US-09-248-796A-18964	Sequence 18964, A
7	116	4.7	989	4	US-09-248-796A-19109	Sequence 19109, A
8	112.5	4.6	685	4	US-09-248-796A-20197	Sequence 20197, A
9	111.5	4.5	986	4	US-09-248-796A-19088	Sequence 19088, A
10	109	4.4	534	4	US-09-248-796A-19568	Sequence 19568, A
11	108.5	4.4	314	4	US-09-248-796A-18676	Sequence 18676, A
12	108	4.4	835	4	US-09-252-991A-32121	Sequence 32121, A
13	107	4.4	479	4	US-09-248-796A-17560	Sequence 17560, A
14	106.5	4.3	775	2	US-08-714-070A-1	Sequence 1, Appli
15	106	4.3	971	4	US-09-248-796A-19531	Sequence 19531, A
16	104	4.2	335	4	US-09-248-796A-17099	Sequence 17099, A
17	104	4.2	1341	4	US-09-949-016-6890	Sequence 6890, Ap
18	104	4.2	1344	4	US-09-949-016-10925	Sequence 10925, A
19	102.5	4.2	808	4	US-09-248-796A-18679	Sequence 18679, A
20	101.5	4.1	351	4	US-09-248-796A-20887	Sequence 20887, A
21	101.5	4.1	421	4	US-09-248-796A-19591	Sequence 19591, A
22	101	4.1	515	4	US-09-252-991A-22451	Sequence 22451, A
23	101	4.1	1587	4	US-09-845-583A-10	Sequence 10, Appl
24	101	4.1	1587	4	US-09-561-709B-3	Sequence 3, Appli
25	100	4.1	758	4	US-10-029-180-92	Sequence 92, Appl
26	99	4.0	1065	4	US-09-538-092-84	Sequence 84, Appl
27	98.5	4.0	309	4	US-10-029-180-98	Sequence 98, Appl
28	98	4.0	263	4	US-09-248-796A-19569	Sequence 19569, A
29	98	4.0	397	4	US-10-029-180-40	Sequence 40, Appl
30	97	3.9	109	4	US-09-248-796A-19570	Sequence 19570, A
31	97	3.9	519	4	US-09-248-796A-19293	Sequence 19293, A
32	96.5	3.9	621	4	US-09-248-796A-18751	Sequence 18751, A
33	96	3.9	694	4	US-10-029-180-22	Sequence 22, Appl
34	95.5	3.9	311	4	US-10-029-180-12	Sequence 12, Appl
35	95	3.9	232	4	US-09-248-796A-18894	Sequence 18894, A
36	95	3.9	461	4	US-09-248-796A-19247	Sequence 19247, A
37	95	3.9	1102	4	US-09-358-383C-36	Sequence 36, Appl
38	95	3.9	1702	4	US-09-854-133-434	Sequence 434, App
39	95	3.9	2052	3	US-09-045-201-2	Sequence 2, Appli
40	95	3.9	2052	3	US-09-619-062-2	Sequence 2, Appli
41	94.5	3.8	205	4	US-09-248-796A-18923	Sequence 18923, A
42	94.5	3.8	756	4	US-09-248-796A-19209	Sequence 19209, A
43	94	3.8	412	2	US-08-755-584-2	Sequence 2, Appli
44	94	3.8	412	3	US-09-192-611-2	Sequence 2, Appli
45	94	3.8	412	4	US-08-755-592A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-029-180-104
; Sequence 104, Application US/10029180
; Patent No. 6806082
; GENERAL INFORMATION:
;   APPLICANT: Cali, Brian M.
;   APPLICANT: Holtzman, Doug
;   APPLICANT: Madden, Kevin T.
;   APPLICANT: Milna, G. Todd
;   APPLICANT: Sherman, Amir
;   APPLICANT: Silva, Jeffry C.
;   APPLICANT: Trueheart, Josh
;   APPLICANT: Zhang, Lixin
;   TITLE OF INVENTION: No. 68060082el Regulators of Fungal Gene Expression
;   FILE REFERENCE: MIC-004
;   CURRENT APPLICATION NUMBER: US/10/029,180
;   CURRENT FILING DATE: 2001-12-22
;   PRIOR APPLICATION NUMBER: US 60/257,431
;   PRIOR FILING DATE: 2000-12-22
;   NUMBER OF SEQ ID NOS: 138
;   SOFTWARE: FastSEQ for Windows Version 4.0
;   SEQ ID NO 104
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fungal gene
US-10-029-180-104

Query Match   6.4%;   Score 157.5; DB 4;   Length 424;
Best Local Similarity   20.6%; Pred. No. 2.1e-07;
Matches 94; Conservative 62; Mismatches 161; Indels 139; Gaps 22;

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Qy   32  RRSCRDRCHAQKIKCTGNKEVTGRAPCQRCQQAGLRCVYSERCPKRKLRQSRA----------  83
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Db    7  RHACDRCHGQKLRCIH---SGGGPCVRCAKAKATCSWSQSLRSNRLKRHNAPISDVPLA  62

Qy   84  -ADLVSADPDP-----------CLHMSSP----------------------PVPSQSLPLDVS-ES  114
              ||| |     ::|                              ||| |:
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Qy  115  HSSNTSRQFLDPPDSYDWSWTSIGT------------DEAIDTDCWGLSQCDGGFSCQLEP  163
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Db  123  ETYNVGHTEADLPATADWMPAVANGPVQTTPPANWQOAFNQE-WAM-----MASOHPV  175

Qy  164  TLPDLPSPFESTVEKAPLPPVSSDIARAASAQRELFDDLSA-------VSQELEBILLAV  216
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Db  176  ATMDTPSR-TSPVSDAVDPPKTVCLLATIRELSELNVDLYAHEATVPRPPASLEE-----  229

Qy  217  TVEWPKQEIWTHPIGMFFNASRRLLTVLRQQ------AQADCHQGT----------  256
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OM protein - protein search, using sw model

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Run on: February 15, 2005, 02:03:56 ; Search time 133 Seconds
(without alignments)
1152.221 Million cell updates/sec

Title: US-09-974-760B-91
Perfect score: 2456
Sequence: 1 MAADQGIFTNSVTLSPVEGS.........FSLARKHGHGMLRDLNNIPP 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376809

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 95%
Listing first 45 summaries

Database :   Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1858.5	75.7	366	16	US-10-402-056-105	Sequence 105, App
2	830	33.8	459	10	US-09-836-705-42	Sequence 42, Appl
3	157.5	6.4	424	13	US-10-029-180-104	Sequence 104, App
4	157.5	6.4	424	15	US-10-149-310-302	Sequence 302, App
5	154.5	6.3	919	15	US-10-369-493-1435	Sequence 1435, Ap
6	154.5	6.3	919	15	US-10-149-310-238	Sequence 238, App
7	136	5.5	604	9	US-09-920-581-3	Sequence 3, Appli
8	136	5.5	604	14	US-10-371-421-3	Sequence 3, Appli
9	136	5.5	604	15	US-10-149-310-46	Sequence 46, Appl
10	135	5.5	433	9	US-09-801-368-38	Sequence 38, Appl
11	135	5.5	433	15	US-10-149-310-30	Sequence 30, Appl
12	132	5.4	1170	15	US-10-369-493-22259	Sequence 22259, A
13	132	5.4	1170	15	US-10-149-310-198	Sequence 198, App
14	131.5	5.4	480	15	US-10-149-310-88	Sequence 88, Appl
15	130.5	5.3	662	9	US-09-801-368-42	Sequence 42, Appl
16	130.5	5.3	662	15	US-10-149-310-44	Sequence 44, Appl
17	130.5	5.3	792	16	US-10-468-250A-110	Sequence 130, App
18	129.5	5.3	579	15	US-10-149-310-42	Sequence 42, Appl
19	126	5.1	821	16	US-10-468-250A-128	Sequence 128, App
20	124.5	5.1	736	15	US-10-149-310-92	Sequence 92, Appl
21	124	5.0	984	15	US-10-149-310-118	Sequence 118, App
22	123.5	5.0	437	15	US-10-149-310-28	Sequence 28, Appl
23	123.5	5.0	607	15	US-10-149-310-274	Sequence 274, App
24	122	5.0	821	15	US-10-149-310-36	Sequence 36, Appl
25	122	5.0	821	16	US-10-468-250A-122	Sequence 122, App
26	121.5	4.9	964	15	US-10-149-310-256	Sequence 256, App
27	121	4.9	470	15	US-10-149-310-284	Sequence 284, App
28	121	4.9	739	9	US-09-801-368-396	Sequence 396, App
29	121	4.9	739	15	US-10-149-310-214	Sequence 214, App
30	121	4.9	821	16	US-10-468-250A-125	Sequence 125, App
31	120.5	4.9	795	16	US-10-468-250A-129	Sequence 129, App
32	120	4.9	470	15	US-10-149-310-160	Sequence 160, App
33	119	4.8	470	15	US-10-149-310-168	Sequence 168, App
34	119	4.8	565	15	US-10-149-310-188	Sequence 188, App
35	118.5	4.8	857	15	US-10-149-310-80	Sequence 80, Appl
36	118.5	4.8	2016	17	US-10-488-056-52	Sequence 52, Appl
37	117	4.8	473	15	US-10-149-310-170	Sequence 170, App
38	117	4.8	767	15	US-10-149-310-90	Sequence 90, Appl
39	116.5	4.7	377	9	US-09-853-386-74	Sequence 74, Appl
40	116.5	4.7	444	15	US-10-149-310-34	Sequence 34, Appl
41	116.5	4.7	882	15	US-10-149-310-122	Sequence 122, App
42	116.5	4.7	1445	15	US-10-149-310-110	Sequence 110, App
43	116	4.7	470	15	US-10-149-310-164	Sequence 164, App
44	115.5	4.7	384	15	US-10-149-310-32	Sequence 32, Appl
45	115	4.7	517	9	US-09-801-368-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-10-402-056-105
; Sequence 105, Application US/10402056
; Publication No. US20040191877A1
GENERAL INFORMATION:
; APPLICANT: Roberts, Shannon
; APPLICANT: Sherman, Amir
; APPLICANT: Trueheart, Joshua
; APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-029001
; CURRENT APPLICATION NUMBER: US/10/402,056
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/32248
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/974,760
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/328,339
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated variant
US-10-402-056-105

Query Match   75.7%;   Score 1858.5;   DB 16;   Length 366;
Best Local Similarity   77.6%;   Pred. No. 1.4e-159;
Matches 364;   Conservative 1;   Mismatches 1;   Indels 103;   Gaps 1;

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Qy  1 MAADQGIFTNSVTLSPVEGSRTGGTLPRRAFRRSCDRCHAQKIKCTGNKEVTGRAPCQRC 60
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Db  1 MAADQGIFTNSVTLSPLEGSRTGGTLPRRAFRRSCDRCLAQKIKCTGNKEVTGRAPCQRC 60
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OM protein - protein search, using sw model

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            GenCore version 5.1.6
     Copyright (c) 1993 - 2005 Compugen Ltd.
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Run on: February 15, 2005, 01:55:19 ; Search time 40 Seconds
(without alignments)
1128.142 Million cell updates/sec

Title: US-09-974-760B-91
Perfect score: 2456
Sequence: 1 MAADQGIFTNSVTLSPVEGS.........FSLARKHGHGMLRDLNNIPP 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 95%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	154.5	6.3	919	2	S45889	probable regulator
2	136	5.5	604	2	JC7252	transcription acti
3	135	5.5	433	2	S69999	sterigmatocystin s
4	132	5.4	1170	2	S30010	probable finger pr
5	131.5	5.4	480	2	T38582	hypothetical funga
6	124.5	5.1	768	2	T37601	probable trancript
7	123.5	5.0	607	2	S63395	probable membrane
8	121.5	4.9	964	2	S48404	probable membrane
9	121	4.9	470	2	S58826	hypothetical prote
10	119	4.8	648	2	T20144	hypothetical prote
11	118.5	4.8	857	2	T40024	probable transcrip
12	117	4.8	473	1	RGBYM3	regulatory protein
13	117	4.8	767	2	T41344	probable zinc-fing
14	116.5	4.7	1445	2	T14913	CAT8 protein - yea
15	115	4.7	6420	2	T30283	polyketide synthas
16	113.5	4.6	650	2	JC7937	transcription acti
17	110.5	4.5	827	2	T39608	zinc finger transc
18	110	4.5	909	2	T06635	hypothetical prote
19	109	4.4	1349	2	T13031	nucleoporin -frui
20	109	4.4	1365	2	T13991	nucleoporin 154 -
21	106.5	4.3	775	2	S41962	thiamin repressibl
22	106.5	4.3	867	2	T41308	hypothetical zinc-
23	106.5	4.3	5327	2	T13564	microtubule-associ
24	106	4.3	743	2	T40521	hypothetical prote
25	106	4.3	1433	2	S54587	CAT8 protein - yea
26	105	4.3	997	2	A60076	230k bullous pemph
27	104.5	4.3	1171	2	T00380	KIAA0637 protein -
28	104	4.2	1280	2	T00365	hypothetical prote
29	104	4.2	1587	2	G86467	hypothetical prote
30	103	4.2	704	2	T50303	hypothetical prote
31	103	4.2	765	2	A36332	regulatory protein
32	102.5	4.2	758	2	S46625	finger protein YJL
33	102.5	4.2	2232	2	T34434	hypothetical prote
34	102	4.1	468	2	S46179	regulatory protein
35	101.5	4.1	1403	2	S24548	homeotic protein p
36	101	4.1	1176	2	T49482	hypothetical prote
37	100.5	4.1	1068	2	S64015	pleiotropic drug r
38	100	4.1	736	2	T06757	hypothetical prote
39	99.5	4.1	547	2	T39478	zinc-finger protei
40	99	4.0	913	2	S61580	probable membrane
41	99	4.0	1048	2	H87721	protein ZC123.2 (i
42	99	4.0	1065	2	S19482	hypothetical prote
43	99	4.0	1425	2	E89303	protein C47E8.8 (i
44	99	4.0	1675	2	T31473	hypothetical prote
45	98.5	4.0	1095	2	T00329	hypothetical prote

ALIGNMENTS

RESULT 1
S45889
probable regulatory protein YBR033w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR0318
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 16-Aug-2004
C;Accession: S45889; S46562
R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45875
A;Accession: S45889
A;Molecule type: DNA
A;Residues: 1-919 <GRI>
A;Cross-references: UNIPROT:P38073; EMBL:Z35902; NID:g536247; PIDN:CAA84975.1; PID:g53
A;Experimental source: strain S288C
R;Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A;Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II f
ly identified genes and a homologue of the SCO1 gene.
A;Reference number: S46551; MUID:94378725; PMID:8091864
A;Accession: S46562
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-919 <SMI>
A;Cross-references: EMBL:X76078; NID:g498748; PIDN:CAA53688.1; PID:g498760
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
C;Genetics:
A;Cross-references: SGD:S0000237
A;Map position: 2R
A;Note: YBR033w
C;Superfamily: GAL4 zinc binuclear cluster homology
C;Keywords: DNA binding; transmembrane protein; zinc finger
F;51-90/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F;56-85/Region: zinc finger
F;408-424/Domain: transmembrane #status predicted <TM1>
F;482-504/Domain: transmembrane #status predicted <TM2>
F;547-563/Domain: transmembrane #status predicted <TM3>
F;703-720/Domain: transmembrane #status predicted <TM4>
F;790-806/Domain: transmembrane #status predicted <TM5>

Query Match   6.3%;   Score 154.5;   DB 2;   Length 919;
Best Local Similarity   23.1%;   Pred. No. 0.0012;
Matches   82; Conservative 52; Mismatches 142; Indels 79; Gaps 14;

```
Qy   2 AADQGIFTNSVTLSPVEGSRTGGTLPRRAFRRSCDRCHAQKIKCTGNKEVTGRAPCQRCQ   61
                ||: .||  ||||| .| .||| :   | :|  ||| ||||
Db  23 SASMGEVNQSVSSRNCERGSEKGTKQRKKASHACDQCRRKRIKCRFDKH-TG--VCQGCL   79

Qy  62 QAGLRC---VYSERCPKRKLRQSRAADLVSADPDP------------CL   95
              |  |          || :|| || | |||
Db  80 EVGEKCQFIRVPLKRGPAKKRGSVVSIEKFSSDNDPLQYRPRTHSYPMNSGNNYLPSLAR  139
```

```
OM protein - protein search, using sw model
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:  February 15, 2005, 01:47:14 ; Search time 173 Seconds
                                          (without alignments)
                                    1388.238 Million cell updates/sec

Title:          US-09-974-760B-91
Perfect score:  2456
Sequence:     1 MAADQGIFTNSVTLSPVEGS.........FSLARKHKHGMLRDLNNIPP 469

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:  1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:   1612377

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 95%
                 Listing first 45 summaries

Database :  UniProt 03:*
            1: uniprot_sprot:*
            2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                      SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	830	33.8	459	2	Q8J0F2	Q8J0F2 penicillium
2	161.5	6.6	1010	2	Q7S6Q4	neurospora
3	158	6.4	478	2	Q6BPX4	debaryomyces
4	154.5	6.3	919	1	YBO3_YEAST	saccharomyc
5	148.5	6.0	500	2	O60877	leptosphaer
6	145.5	5.9	1082	2	Q6CXE0	kluyveromyc
7	145	5.9	603	2	Q7SEM4	neurospora
8	142.5	5.8	520	2	Q8X0T1	neurospora
9	138.5	5.6	554	2	Q7SAV4	neurospora
10	137	5.6	-1287	2	Q6FLP2	candida gla
11	136	5.5	604	2	O60201	aspergillus
12	135.5	5.5	442	2	Q8TG81	aspergillus
13	135	5.5	433	1	AFLR_EMENI	emericella
14	133.5	5.4	922	2	Q6FXI8	candida gla
15	133	5.4	1254	2	Q6FJW6	candida gla
16	133	5.4	470	2	Q9UVH4	saccharomyc
17	132	5.4	1170	1	YKD8_YEAST	saccharomyc
18	131.5	5.4	480	2	O94392	schizosacch
19	130.5	5.3	662	2	Q9Y728	emericella
20	130.5	5.3	785	2	Q672V8	aspergillus
21	130	5.3	436	2	Q6iWF3	aspergillus
22	129.5	5.2	579	2	Q9Y8A1	aspergillus
23	128.5	5.2	442	2	Q8TG77	aspergillus
24	128.5	5.2	442	2	Q8TG79	aspergillus
25	128.5	5.2	442	2	Q8TG84	aspergillus
26	127	5.2	832	2	Q6FUL5	candida gla
27	126.5	5.2	341	1	ACE2_TRIRE	trichoderma
28	126.5	5.2	442	2	Q8TFC7	aspergillus
29	126.5	5.2	442	2	Q8TG78	aspergillus
30	126.5	5.2	442	2	Q8TG86	aspergillus
31	126.5	5.2	1353	2	Q7S6K8	neurospora
32	125.5	5.1	442	2	Q8TG82	aspergillus
33	124.5	5.1	442	2	Q8TG83	aspergillus
34	124.5	5.1	442	2	Q8TG87	aspergillus
35	124	5.0	984	2	O94167	glomerella
36	123.5	5.0	437	2	AFLR_ASPFL	aspergillus
37	123.5	5.0	444	2	Q8TG71	aspergillus
38	123.5	5.0	607	1	YN92_YEAST	saccharomyc
39	123	5.0	444	2	Q8TG72	aspergillus
40	122	5.0	441	2	Q8TG80	aspergillus
41	122	5.0	444	2	Q8J2V0	aspergillus
42	122	5.0	444	2	Q874B8	aspergillus
43	122	5.0	821	1	ALCR_EMENI	emericella
44	121.5	4.9	964	1	YINO_YEAST	saccharomyc
45	121	4.9	444	2	Q8TFC9	aspergillus

```
                      ALIGNMENTS

RESULT 1
Q8J0F2
ID   Q8J0F2       PRELIMINARY;      PRT;   459 AA.
AC   Q8J0F2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Transcription factor.
GN   Name=mlcR;
OS   Penicillium citrinum.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX   NCBI_TaxID=5077;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22162865; PubMed=12172803; DOI=10.1007/s00438-002-0697-y;
RA   Abe Y., Suzuki T., Ono C., Iwamoto K., Hosobuchi M., Yoshikawa H.;
RT   "Effect of increased dosage of the ML-236B (compactin) biosynthetic
RT   gene cluster on ML-236B production in Penicillium citrinum.";
RL   Mol. Genet. Genomics 268:130-137(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22227327; PubMed=12243508; DOI=10.1007/s00438-002-0736-8;
RA   Abe Y., Suzuki T., Mizuno T., Ono C., Iwamoto K., Hosobuchi M.,
RA   Yoshikawa H.;
RT   "Molecular cloning and characceization of an ML-236B (compactin)
RT   biosynthetic gene cluster in Penicillium citrinum.";
RL   Mol. Genet. Genomics 267:636-646(2002).
DR   EMBL; AB072893; BAC20569.1;
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR001138; Fungi_Trscrp_N.
DR   Pfam; PF00172; Zn_clus; 1.
DR   PRINTS; PR00054; FUNGALZNCYS.
DR   SMART; SM00066; GAL4; 1.
DR   PROSITE; PS00463; ZN2_CY6_FUNGAL_1; UNKNOWN_1.
DR   PROSITE; PS50048; ZN2_CY6_FUNGAL_2; 1.
KW   DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW   Transcription regulation; Zinc.
SQ   SEQUENCE  459 AA;  50356 MW;  4D2D1B3307EF46C1 CRC64;

Query Match             33.8%;  Score 830;  DB 2;  Length 459;
Best Local Similarity   42.3%;  Pred. No. 3.3e-54;
Matches  196;  Conservative  62;  Mismatches 153;  Indels  54;  Gaps  9;

Qy         26 LPRRAFRRSCDRCHAQKIKCTGNKEVTGRAPCQRCQQAGLRCVYSERCPKRKLRQSRAA- 84
              ||||||||||||||||  |||| ||   |  |||||||||||||||||  ||| : ||
Db         12 LRRRAFRRSCDRCHAQLKCTGSNANLVRAQCQRCQQAGLRCVYSERLPKRNLHKEAAAG 71
```

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2005, 20:20:52 ; Search time 5100 Seconds
(without alignments)
4455.980 Million cell updates/sec

Title: US-09-974-760B-91
Perfect score: 2456
Sequence: 1 MAADQGIFTNSVTLSPVEGS.........FSLARKHGHGMLRDLNNIPP 469

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters: 9416463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 95%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09974760/runat_14022005_160342_6751/app_query.fasta_1.647
-DB=GenEmbl -QFMT=fastap -SUFFIX=95pct.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=95 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974760 @CGN_1_1_5600 @runat_14022005_160342_6751 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.		Score	% Query Match	Length	DB	ID	Description
1		830	33.8	1380	6	BD178141	BD178141 On the st
2	c	811	33.0	34203	6	BD178102	BD178102 On the st
3	c	811	33.0	34203	6	BD178103	BD178103 On the st
4	c	811	33.0	34203	6	BD013765	BD013765 ML-236B b
5	c	811	33.0	34203	6	BD013766	BD013766 ML-236B b
6	c	811	33.0	34203	6	BD093553	BD093553 DNAs rela
7	c	811	33.0	38231	8	BD093554	BD093554 DNAs rela
8	c	811	33.0	38231	8	AB072893	AB072893 Penicilli
9	c	292.5	11.9	562	6	BD178135	BD178135 On the st
10	c	292.5	11.9	562	6	BD013798	BD013798 ML-236B b
11		266.5	10.9	562	6	BD093586	BD093586 DNAs rela
12		266.5	10.9	541	6	BD178123	BD178123 On the st
13		266.5	10.9	541	6	BD013786	BD013786 ML-236B b
14		266.5	10.9	541	6	BD093574	BD093574 DNAs rela
15		163	6.6	2757	6	AX684918	AX684918 Sequence
16		163	6.6	3114	8	SCYBR033W	Z35902 S.cerevisia
17		163	6.6	33117	8	SCGAL1	X76078 S.cerevisia
18	c	161	6.6	68683	8	AY553235	AY53235 Leptospha
19		158	6.4	110000	8	CR382137_07	Continuation (8 of
20		157.5	6.4	1272	6	AX505237	AX505237 Sequence
21		157.5	6.4	1272	6	AX684982	AX684982 Sequence
22		153.5	6.2	1440	6	AX684768	AX684768 Sequence
23		153.5	6.2	11578	8	SPAC2H10	AL034486 S.pombe c
24		146	5.9	241050	2	AC119506	AC119506 Rattus no
25	c	146	5.9	244250	2	AC095307	AC095307 Rattus no
26	c	145.5	5.9	110000	8	CR382121_07	Continuation (8 of
27	c	145.5	5.9	110000	8	CR382121_08	Continuation (9 of
28		145	5.9	35745	3	LMFL5174	AL445944 Leishmani
29		143.5	5.8	3667	3	AK110197	AK110197 Oryza sat
30	c	143.5	5.8	261960	2	AC120634	AC120634 Rattus no
31		140.5	5.7	1812	6	AX684724	AX684724 Sequence
32		140	5.7	2045	8	AF441422	AF441422 Aspergill
33		140	5.7	2051	8	AF441414	AF441414 Aspergill
34		140	5.7	110000	1	AP006487_2	Continuation (3 of
35		140	5.7	301950	1	AP006570	AP006570 Globeobact
36		139.5	5.7	110000	8	CR380958_02	Continuation (3 of
37		139.5	5.7	245684	2	AC098110	AC098110 Rattus no
38	c	139.5	5.7	255473	2	AC121416	AC121416 Rattus no
39		139	5.7	3980	6	AR309623	AR309623 Sequence
40		139	5.7	3986	8	AR309624	AR309624 Sequence
41		139	5.7	3986	8	AOAJ5258	AJ005258 Aspergill
42		139	5.7	8813	8	AB012945	AB012945 Aspergill
43	c	139	5.7	35244	3	AB021876	AB021876 Aspergill
44	c	138.5	5.6	1934	3	LTALDDE	231698 L.tarentola
45	c	138.5	5.6	301675	1	AP005027	AP005027 Streptomy

ALIGNMENTS

RESULT 1
BD178141
LOCUS   BD178141   1380 bp   DNA   linear   PAT 16-APR-2003
DEFINITION   On the structural gene of gene cluster.
ACCESSION   BD178141
VERSION   BD178141.1 GI:30015405
KEYWORDS   JP 2002315579-A/40.
SOURCE   Penicillium citrinum
ORGANISM   Penicillium citrinum
             Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
             Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE   1 (bases 1 to 1380)
AUTHORS   Abe,Y., Ono,C. and Yoshikawa,H.
TITLE   On the structural gene of gene cluster
JOURNAL   Patent: JP 2002315579-A 40 29-OCT-2002;
             SANKYO CO LTD
COMMENT   OS   Penicillium citrinum
             PN   JP 2002315579-A/40
             PD   29-OCT-2002
             PF   18-APR-2001 JP 2001119385
             PI   YUKI ABE,CHIHO ONO,HIROJI YOSHIKAWA
             PC   C12N15/09,C12N1/15,C12N1/21,C12P17/06//(C12N1/15,C12R1:80), PC
                  (C12P17/06,C12R1:80),C12N15/00
             CC   On the structural gene of gene cluster
             FH   Key   Location/Qualifiers
             FT   CDS   (1)..(1380).
FEATURES   Location/Qualifiers
     source   1..1380

OM protein - nucleic search, using frame_plus_p2n model

```
                    GenCore version 5.1.6
            Copyright (c) 1993 - 2005 Compugen Ltd.
```

Run on: February 16, 2005, 19:56:52 ; Search time 643 Seconds
(without alignments)
4317.821 Million cell updates/sec

Title: US-09-974-760B-91
Perfect score: 2456
Sequence: 1 MADQGIFTNSVTLSPVEGS.........FSLARKHKHGMLRDLNNIPP 469

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop   6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780382

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 95%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool_p/US09974760/runat_14022005_160342_6744/app_query.fasta_1.647
-DB=N Geneseq_16Dec04 -QFMT=fastap -SUFFIX=95pct.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=95 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09974760 @CGN_1_1_708 @runat_14022005_160342_6744 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04.*
   1: geneseqm1980s.*
   2: geneseqm1990s.*
   3: geneseqm2000s.*
   4: geneseqm2001as.*
   5: geneseqm2001bs.*
   6: geneseqm2002as.*
   7: geneseqm2002bs.*
   8: geneseqm2003as.*
   9: geneseqm2003bs.*
  10: geneseqm2003cs.*
  11: geneseqm2003ds.*
  12: geneseqm2004as.*
  13: geneseqm2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	830	33.8	1377	10	ADE81190	Ade81190 MlcR codi
	2	830	33.8	1380	6	AAS16808	Aas16808 Penicilli
c	3	811	33.0	34203	4	AAF74546	Aaf74546 Penicilli
	4	811	33.0	34203	6	AAS16770	Aas16770 Penicilli
c	5	811	33.0	34263	4	AAF74547	Aaf74547 Penicilli
c	6	811	33.0	72149	10	ADE81173	ML-236B s
c	7	292.5	11.9	562	4	AAF74579	ML-236B b
c	8	292.5	11.9	562	6	AAS16802	Penicilli
c	9	266.5	10.9	541	4	AAF74567	ML-236B b
	10	266.5	10.9	541	6	AAS16790	Penicilli
	11	163	6.6	2757	6	ABN79876	Fungal_ZB
	12	163	6.6	2760	13	ADS46692	Bacterial
	13	157.5	6.4	1272	6	ABQ94268	lovF gene
	14	157.5	6.4	1272	6	ABN79908	Fungal_ZB
	15	153.5	6.2	1440	6	ABN79801	Fungal_ZB
	16	140.5	5.7	1812	6	ABN79780	Fungal_ZB
	17	139	5.7	3980	2	AAV03014	Aspergill
	18	135	5.5	1299	6	ABN79772	Fungal_ZB
	19	132.5	5.4	2100	6	AAV31356	Trichoder
	20	132	5.4	1311	6	ABN79771	Fungal_ZB
	21	132	5.4	3510	6	ABN79856	Fungal_ZB
	22	132	5.4	3513	13	ADT47508	Bacterial
	23	130.5	5.3	1986	6	ABN79779	Fungal_ZB
	24	130.5	5.3	2384	6	ABS69979	Aspergill
	25	129.5	5.3	1737	6	ABN79778	Fungal_ZB
	26	129	5.3	1152	6	ABN79773	Fungal_ZB
	27	129	5.3	1332	6	ABN79774	Fungal_ZB
	28	128.5	5.2	1373	6	AAV31355	Trichoder
	29	127.5	5.2	2170	6	ABQ54970	Human ova
c	30	127.5	5.2	5378	13	ADR67197	Human bla
c	31	127.5	5.2	5382	10	ADD14722	Human src
c	32	126.5	5.2	3176	10	ADF81709	Leukaemia
c	33	126.5	5.2	3199	13	ABD32931	Human can
	34	126.5	5.2	3312	13	ABD32932	Human can
	35	126.5	5.2	3996	12	ADQ63000	Novel hum
	36	126.5	5.2	5154	13	ADR10410	Full leng
	37	126.5	5.2	7819	10	ADE71185	Novel hum
	38	126	5.1	2466	6	ABS69975	Aspergill
	39	125.5	5.1	2217	6	ABN79864	Fungal_ZB
	40	124.5	5.1	2208	6	ABN79803	Fungal_ZB
	41	124	5.0	2952	6	ABN79816	Fungal_ZB
	42	123.5	5.0	1821	6	ABN79894	Fungal_ZB
	43	123	5.0	1596	10	ADE81192	Orfl codi
	44	123	5.0	1695	6	ABN79851	Fungal_ZB
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ALIGNMENTS

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AC   ADE81190;
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DT   29-JAN-2004 (first entry)
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DE   MlcR coding sequence, SEQ ID 18.
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KW   ML-236B; HMG-CoA reducing enzyme; ds; MlcR.
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OS   Penicillium citrinum.
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FH   Key           Location/Qualifiers
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XX
PN   JP2003116567-A.
XX
PD   22-APR-2003.
XX
PF   15-OCT-2001; 2001JP-00316578.
XX
PR   15-OCT-2001; 2001JP-00316578.
XX
PA   (SANY ) SANKYO CO LTD.
XX
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2005  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    February 16, 2005, 21:08:47 ; Search time 234 Seconds
                                         (without alignments)
                         3279.546 Million cell updates/sec

Title:          US-09-974-760B-91
Perfect score:  2456
Sequence:       1 MAADQGIFTNSVTLSPVEGS..........FSLARKHXHGMLRDLNNIPP 469

Scoring table:  BLOSUM62
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                Ygapop  10.0 , Ygapext  0.5
                Fgapop   6.0 , Fgapext  7.0
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Searched:       1202784 seqs, 818183359 residues

Total number of hits satisfying chosen parameters:    2405566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 95%
                 Listing first 45 summaries

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 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	157.5	6.4	1272	4	US-10-029-180-103	Sequence 103, App
2	139	5.7	3980	3	US-09-197-814-1	Sequence 1, Appli
3	139	5.7	3980	4	US-09-197-814-2	Sequence 2, Appli
4	139	5.7	3980	4	US-09-920-581-1	Sequence 1, Appli
5	139	5.7	3980	4	US-09-920-581-2	Sequence 2, Appli
c 6	129.5	5.3	49225	4	US-09-902-540-1269	Sequence 1269, Ap
7	127	5.2	2844	4	US-09-669-980A-5	Sequence 5, Appli
8	126.5	5.2	3061	3	US-09-147-119-6	Sequence 6, Appli
9	126.5	5.2	3145	4	US-09-147-119-6	Sequence 2624, Ap
10	121.5	4.9	2970	4	US-09-248-796A-5006	Sequence 5006, Ap
11	121	4.9	110585	4	US-09-949-016-13427	Sequence 13427, A
12	119.5	4.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
13	119.5	4.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	119	4.8	3047	4	US-09-016-434-1465	Sequence 1465, Ap
15	118	4.8	927	4	US-10-029-180-97	Sequence 97, Appl
c 16	118	4.8	1317	4	US-09-248-796A-4861	Sequence 4861, Ap
c 17	118	4.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
18	118	4.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
19	114.5	4.7	2961	4	US-09-248-796A-4985	Sequence 4985, Ap
c 20	113.5	4.6	3226	3	US-08-870-126-10	Sequence 10, Appl
c 21	113.5	4.6	3226	3	US-08-445-247-10	Sequence 10, Appl
22	112.5	4.6	2055	4	US-09-248-796A-6094	Sequence 6094, Ap
23	112.5	4.6	4935	4	US-09-949-016-1019	Sequence 1019, Ap
24	112.5	4.6	4935	4	US-09-949-016-5054	Sequence 5054, Ap
25	112.5	4.6	41062	4	US-09-949-016-12761	Sequence 12761, A
26	112.5	4.6	41062	4	US-09-949-016-16796	Sequence 16796, A
27	112	4.6	109690	4	US-09-949-016-13525	Sequence 13525, A
28	111.5	4.5	44377	2	US-08-804-227C-7	Sequence 7, Appli
29	111.5	4.5	44377	4	US-08-804-198-1	Sequence 1, Appli
c 30	110.5	4.5	792	4	US-09-252-991A-15292	Sequence 15292, A
31	110	4.5	2239	4	US-09-774-528-49	Sequence 49, Appl
32	109.5	4.5	2871	4	US-09-252-991A-11431	Sequence 11431, A
c 33	109.5	4.5	9880	4	US-09-902-540-936	Sequence 936, App
34	109	4.4	1548	4	US-09-252-991A-5880	Sequence 5880, Ap
35	109	4.4	1605	4	US-09-248-796A-5465	Sequence 5465, Ap
36	109	4.4	1735	3	US-09-163-444-3	Sequence 3, Appli
37	108.5	4.4	942	4	US-09-248-796A-4573	Sequence 4573, Ap
38	108.5	4.4	2052	4	US-09-252-991A-12103	Sequence 12103, A
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41	108	4.4	2508	4	US-09-252-991A-15550	Sequence 15550, A
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43	107.5	4.4	4978	4	US-09-902-540-775	Sequence 775, App
c 44	107.5	4.4	7704	4	US-09-902-540-743	Sequence 743, App
c 45	107.5	4.4	10322	4	US-09-902-540-989	Sequence 989, App

ALIGNMENTS

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; Sequence 103, Application US/10029180
; Patent No. 6806082
; GENERAL INFORMATION:
;  APPLICANT: Cali, Brian M.
;  APPLICANT: Holtzman, Doug
;  APPLICANT: Madden, Kevin T.
;  APPLICANT: Milna, G. Todd
;  APPLICANT: Sherman, Amir
;  APPLICANT: Silva, Jeffry C.
;  APPLICANT: Trueheart, Josh
;  APPLICANT: Zhang, Lixin
;  TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression
;  FILE REFERENCE: MIC-004
;  CURRENT APPLICATION NUMBER: US/10/029,180
;  CURRENT FILING DATE: 2001-12-22
;  PRIOR APPLICATION NUMBER: US 60/257,431
;  PRIOR FILING DATE: 2000-12-22
;  NUMBER OF SEQ ID NOS: 138
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 103
;  LENGTH: 1272
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: fungal gene
US-10-029-180-103

Alignment Scores:
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Best Local Similarity:   21.49%          Mismatches:      170
Query Match:             6.41%           Indels:          111
DB:                      4               Gaps:             19
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          Copyright   GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:   February 16, 2005, 22:54:23 ; Search time 673 Seconds
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Title:            US-09-974-760B-91
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Searched:         5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters:       10757281

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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	4	811	33.0	34203	10	US-09-836-705-2	Sequence 2, Appli
c	5	292.5	11.9	562	10	US-09-836-705-34	Sequence 34, Appl
c	6	266.5	10.9	541	10	US-09-836-705-22	Sequence 22, Appl
	7	163	6.6	2757	17	US-10-149-310-237	Sequence 237, App
	8	163	6.6	2760	17	US-10-369-493-25122	Sequence 25122, A
	9	157.5	6.4	1272	13	US-10-029-180-103	Sequence 103, App
	10	157.5	6.4	1272	17	US-10-149-310-301	Sequence 301, App
	11	153.5	6.2	1440	17	US-10-149-310-87	Sequence 87, Appl
	12	140.5	5.7	1812	17	US-10-149-310-45	Sequence 45, Appl
	13	139	5.7	3980	9	US-09-920-581-1	Sequence 1, Appli
	14	139	5.7	3980	9	US-09-920-581-2	Sequence 2, Appli
	15	139	5.7	3980	15	US-10-371-421-1	Sequence 1, Appli
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	18	136	5.5	1557	18	US-10-437-963-92795	Sequence 92795, A
	19	135	5.5	1299	17	US-10-149-310-29	Sequence 29, Appl
	20	135	5.5	1302	9	US-09-801-368-37	Sequence 37, Appl
	21	133.5	5.4	1551	15	US-10-156-761-1622	Sequence 1622, Ap
	22	132	5.4	1311	17	US-10-149-310-27	Sequence 27, Appl
	23	132	5.4	3510	17	US-10-149-310-197	Sequence 197, App
	24	132	5.4	3513	17	US-10-369-493-45946	Sequence 45946, A
	25	130.5	5.3	1986	17	US-10-149-310-43	Sequence 43, Appl
	26	130.5	5.3	1989	9	US-09-801-368-41	Sequence 41, Appl
	27	130.5	5.3	2384	18	US-10-468-250A-78	Sequence 78, Appl
	28	129.5	5.3	1737	17	US-10-149-310-41	Sequence 41, Appl
	29	129	5.3	1152	17	US-10-149-310-31	Sequence 31, Appl
	30	129	5.3	1332	17	US-10-149-310-33	Sequence 33, Appl
c	31	127.5	5.2	2170	17	US-10-264-049-850	Sequence 850, App
	32	127	5.2	2844	19	US-10-943-742-5	Sequence 5, Appl
c	33	126.5	5.2	894	18	US-10-437-963-21580	Sequence 21580, A
	34	126	5.1	2466	18	US-10-468-250A-74	Sequence 74, Appl
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	36	125.5	5.1	2217	17	US-10-149-310-213	Sequence 213, App
	37	125.5	5.1	2220	9	US-09-801-368-395	Sequence 395, App
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ALIGNMENTS

RESULT 1
US-10-402-056-114
; Sequence 114, Application US/10402056
; Publication No. US2004019187A1
; GENERAL INFORMATION:
;   APPLICANT: Roberts, Shannon
;   APPLICANT: Sherman, Amir
;   APPLICANT: Trueheart, Joshua
;   APPLICANT: Milne, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REFERENCE: 14184-029001
; CURRENT APPLICATION NUMBER: US/10/402,056
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/32248
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/974,760
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/328,339
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 118

OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: February 16, 2005, 21:02:37 ; Search time 3602 Seconds
(without alignments)
4956.175 Million cell updates/sec

Title: US-09-974-760B-91
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Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 95%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_gss1:*
9: gb_gss2:*

	Result No.	Score	Query Match	Length	DB	ID	Description	
	1	145.5	5.9	791	7	CF682666	CF682666	CCACQ27TR
	2	143.5	5.8	705	5	BQ110832	BQ110832	VD0205D08
	3	136	5.5	925	7	CO008256	CO008256	EST796591
	4	131	5.3	773	8	CF706713	CF706713	CCAFS59TR
	5	130.5	5.3	570	8	AQ397018	AQ397018	mgxb0021J
	6	129.5	5.3	1503	5	BM918679	BM918679	AGENCOURT
	7	129	5.3	2472	9	CL961584	CL961584	OsIFCC006
	8	127.5	5.2	731	7	CF868238	CF868238	tric014xd
c	9	127.5	5.2	786	6	CB898308	CB898308	tric014xd
	10	127.5	5.2	857	7	CO021754	CO021754	EST817847
c	11	127.5	5.2	2066	9	AY399870	AY399870	Homo sapi
c	12	127.5	5.2	2274	7	CR590353	CR590353	full-leng
	13	126.5	5.2	740	7	CF886493	CF886493	tric030xh
	14	126.5	5.2	812	6	CF902489	CF902489	tric030xh
	15	126.5	5.2	1904	3	BC050362	BC050362	Homo sapi
	16	126.5	5.2	5176	3	CR749286	CR749286	Homo sapi
	17	126	5.1	584	7	CO134902	CO134902	EST829573
	18	126	5.1	623	7	CO022915	CO022915	EST819008
	19	125	5.1	1094	6	CD458335	CD458335	Fg08_09e0
	20	125	5.0	1066	6	CD501980	CD501980	CDA53-H11
	21	123.5	5.0	2786	3	AK082888	AK082888	Mus muscu
	22	123	5.0	925	7	CO021563	CO021563	EST817656
	23	120.5	4.9	750	7	CF877407	CF877407	tric075xp
	24	120.5	4.9	765	7	CF688031	CF688031	CCAI871TR
	25	120.5	4.9	812	6	CB905758	CB905758	tric075xp
	26	120.5	4.9	1272	5	BQ648956	BQ648956	AGENCOURT
	27	120	4.9	706	5	BU063507	BU063507	Fgr_3_D08
	28	119.5	4.9	1530	4	BM543030	BM543030	AGENCOURT
	29	119	4.8	683	7	CF693020	CF693020	CCAAH76TR
	30	119	4.8	695	7	CF870415	CF870415	tric022xn
	31	119	4.8	766	6	CB900596	CB900596	tric022xn
	32	118.5	4.8	858	7	CN809042	CN809042	EST0388_M
	33	118	4.8	759	7	CF869789	CF869789	tric020xh
	34	118	4.8	815	6	CB899935	CB899935	tric020xh
c	35	118	4.8	974	7	CNS03ADZ	AL235088	Tetraodon
	36	117.5	4.8	1632	9	CL945327	CL945327	OsIFSB003
c	37	117.5	4.8	3282	9	CL957631	CL957631	OsIFCC036
	38	117	4.8	658	5	BQ138028	BQ138028	NF012D11P
c	39	117	4.8	735	7	CF714957	CF714957	CCADQ07TF
c	40	117	4.8	818	7	CO141871	CO141871	EST836542
c	41	117	4.8	866	7	CF711138	CF711138	CCAF326TO
c	42	117	4.8	947	5	CC668530	CC668530	OGLAV40TH
	43	116.5	4.7	789	7	CF687839	CF687839	CCAA796TR
	44	116.5	4.7	844	7	CF695274	CF695274	CCADB13TR
	45	116.5	4.7	873	7	CF694730	CF694730	CCA246TR

ALIGNMENTS

RESULT 1
CF682666

LOCUS   CF682666   791 bp   mRNA   linear   EST 16-AUG-2004
DEFINITION   CCACQ27TR C.neoformans strain JEC21 Cryptococcus neoformans var.
             neoformans cDNA clone CCACQ27, mRNA sequence.
ACCESSION   CF682666
VERSION   CF682666.1 GI:41536825
KEYWORDS   EST.
SOURCE   Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
             var. neoformans)
  ORGANISM   Cryptococcus neoformans var. neoformans
             Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
             Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
             Filobasidiella.
REFERENCE   1 (bases 1 to 791)
  AUTHORS   Loftus,B.
  TITLE   End sequencing of clones from a Full length enriched, normalized
             JEC21 cDNA library
  JOURNAL   Unpublished (2003)
COMMENT   Other ESTs: CCACQ27TF
             Contact: Brendan Loftus
             TIGR
             Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
             Rockville, MD 20850, USA
             Tel: 301-838-3543
             Fax: 301-838-0208
             Email: crypt@tigr.org
             Seq primer: TR.
FEATURES   Location/Qualifiers
     source   1..791
                     /organism="Cryptococcus neoformans var. neoformans"
                     /mol_type="mRNA"
                     /strain="JEC21"